

FIG. 1

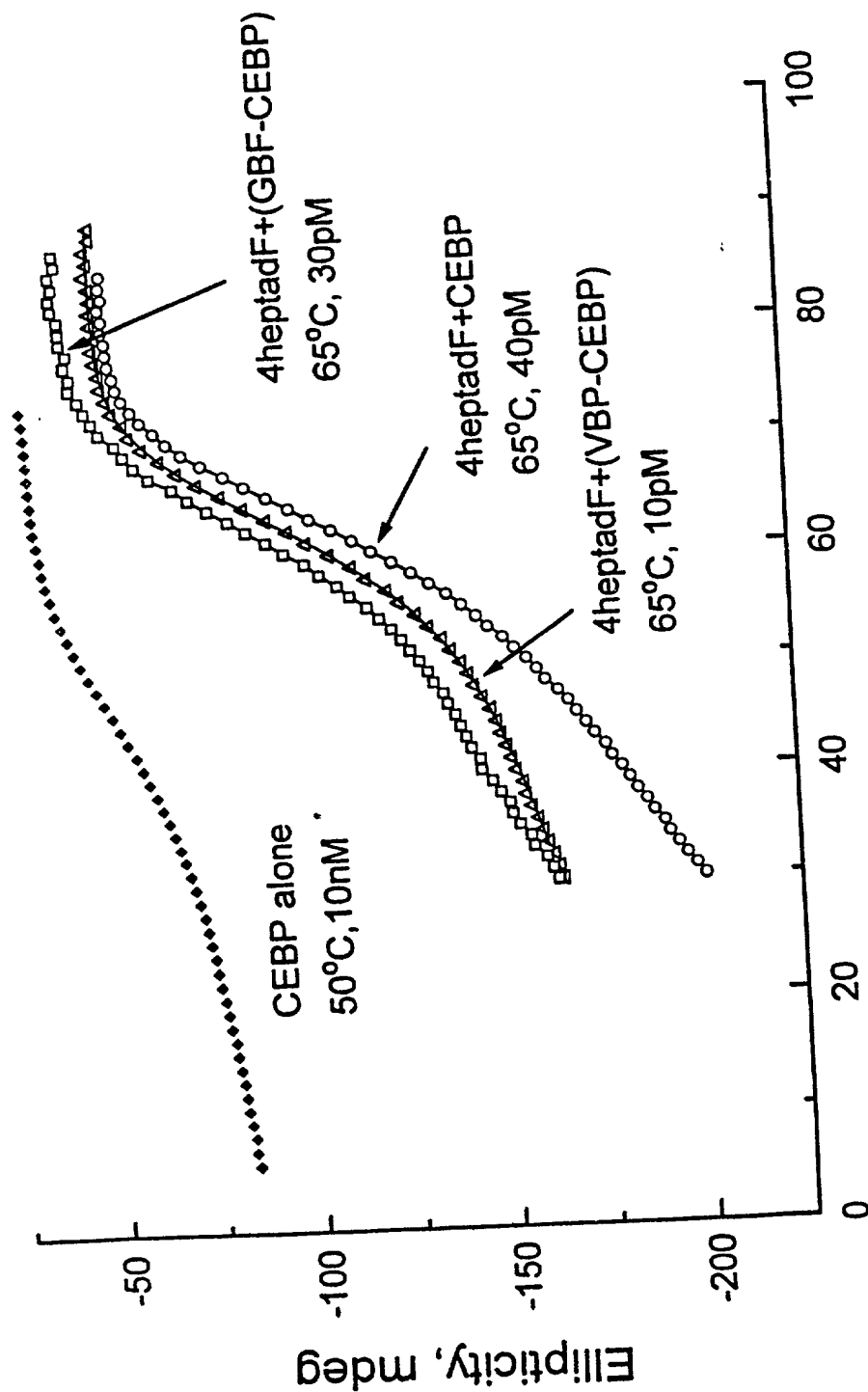


FIG. 2

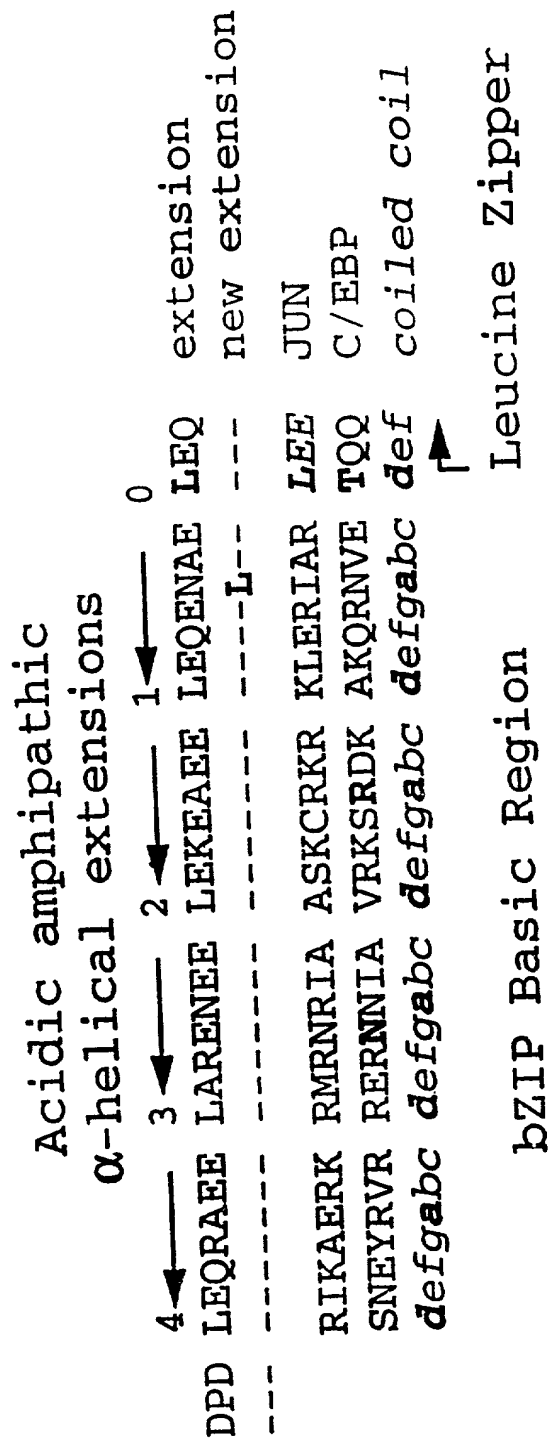


FIG. 3

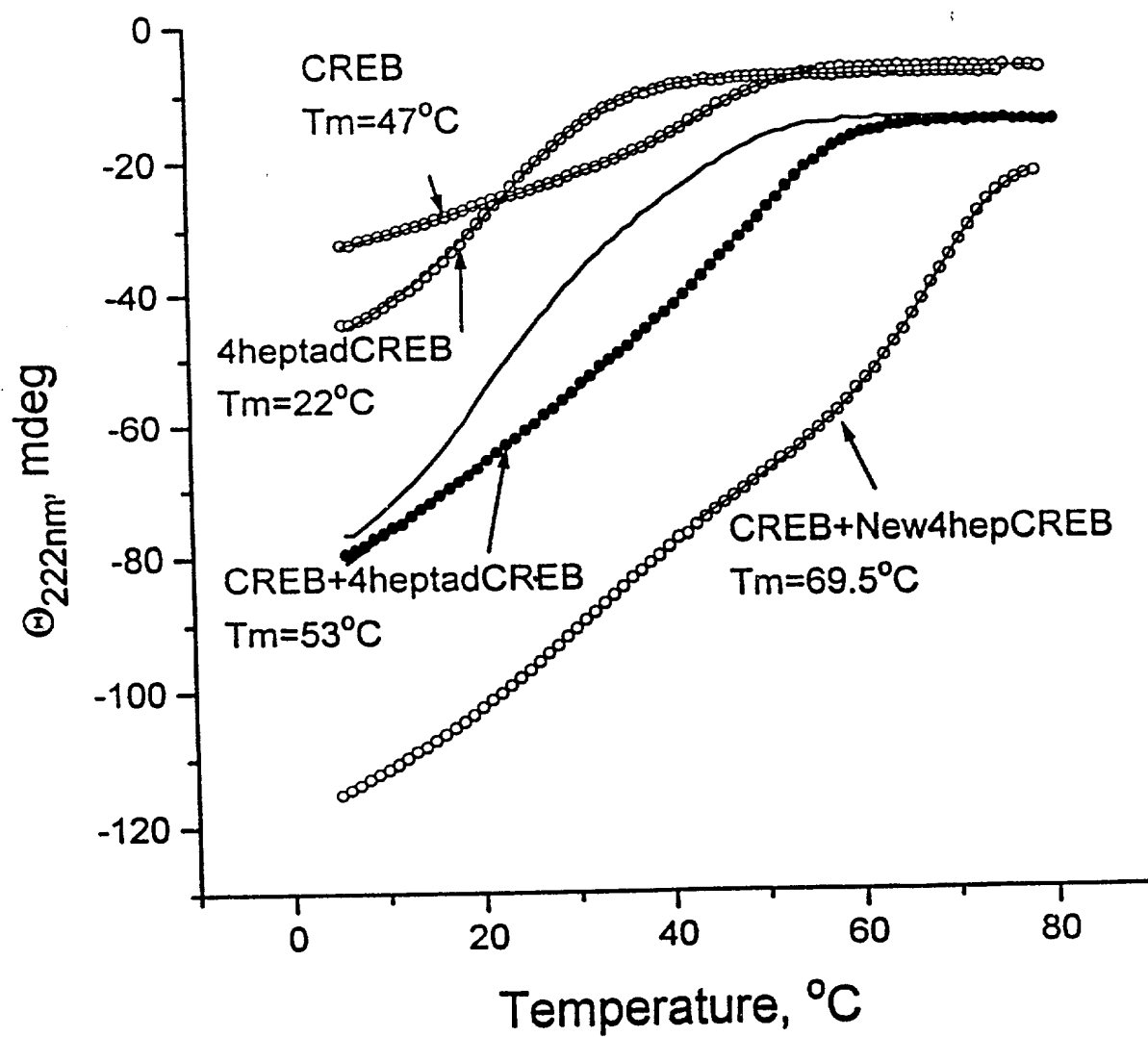


FIG. 4

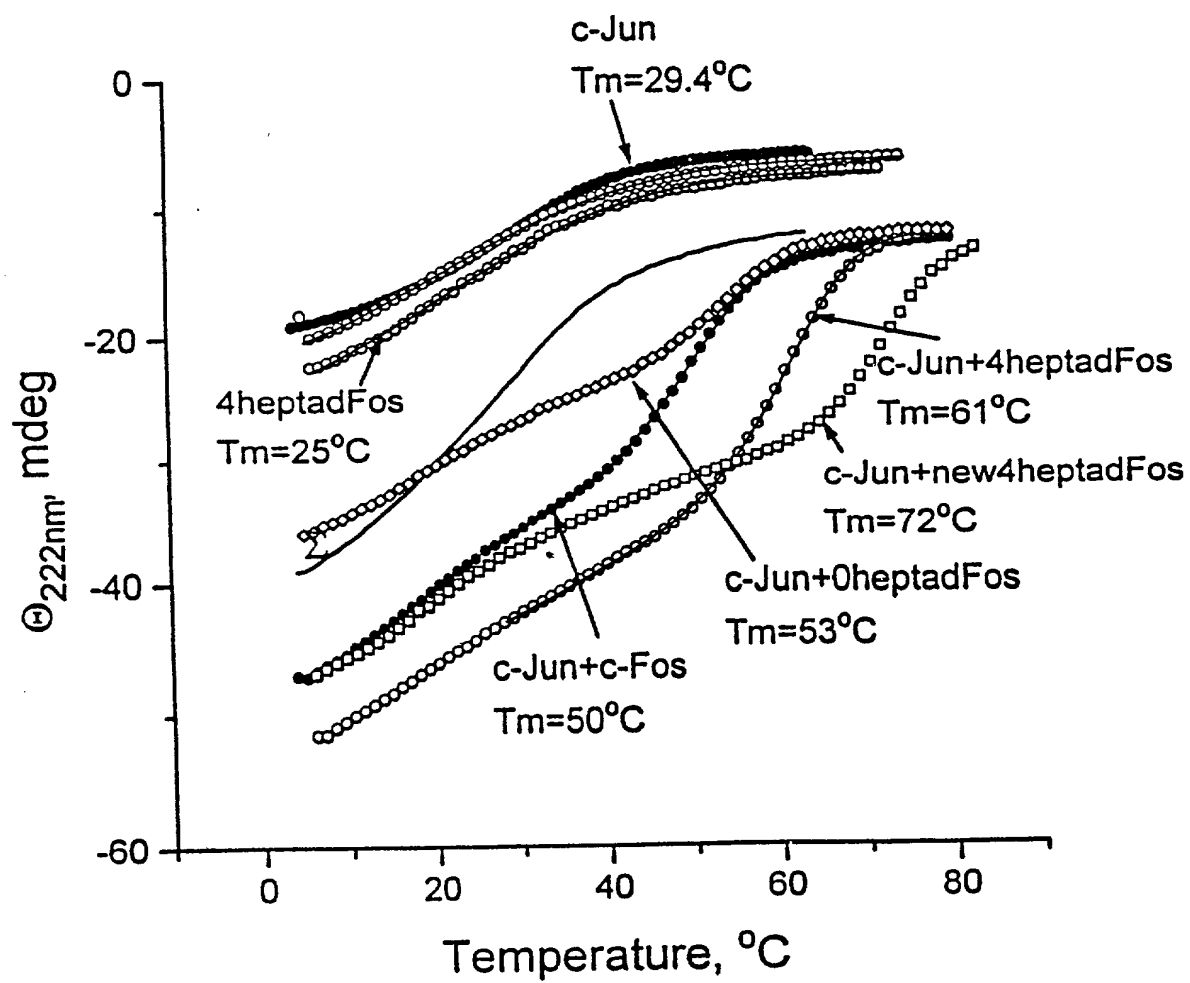


FIG. 5A

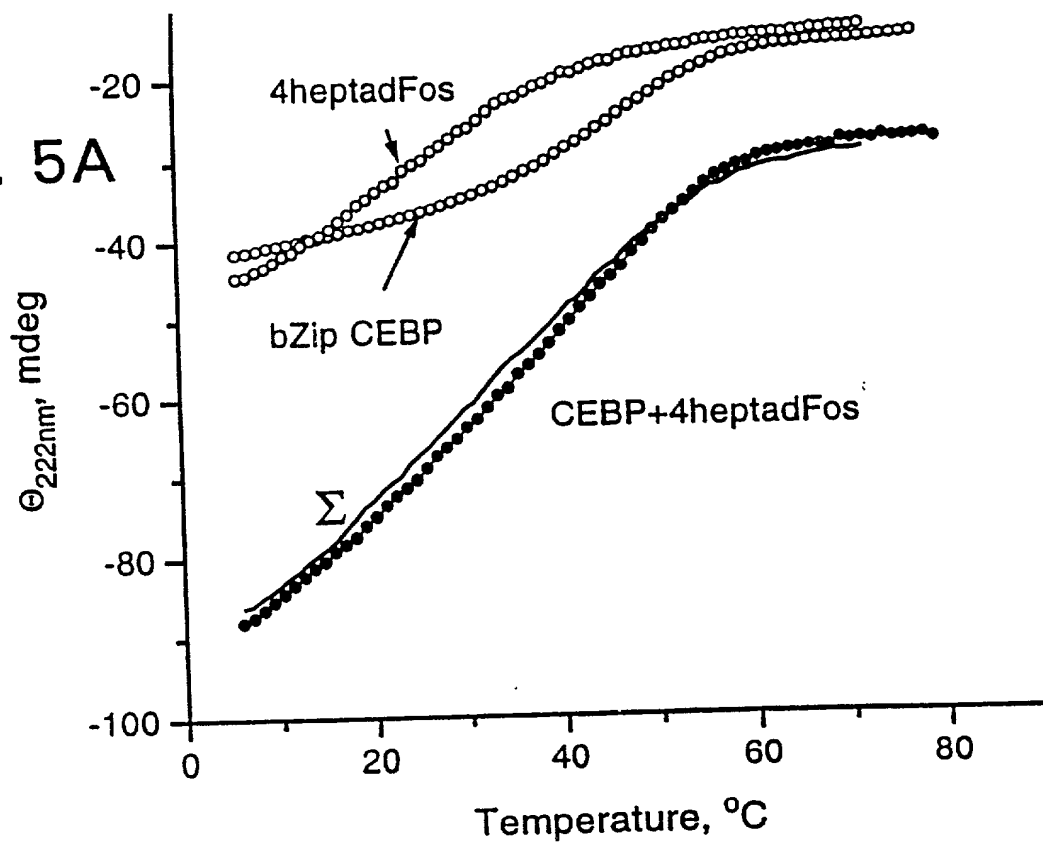


FIG. 5B

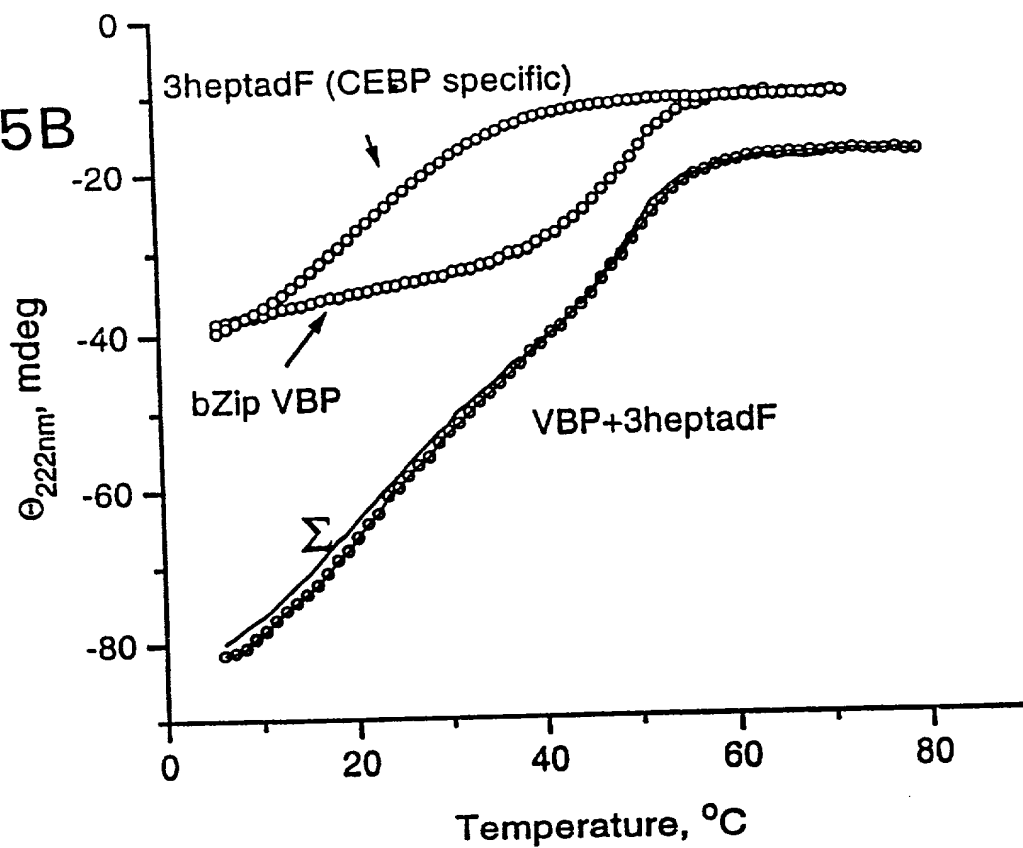


FIG. 6

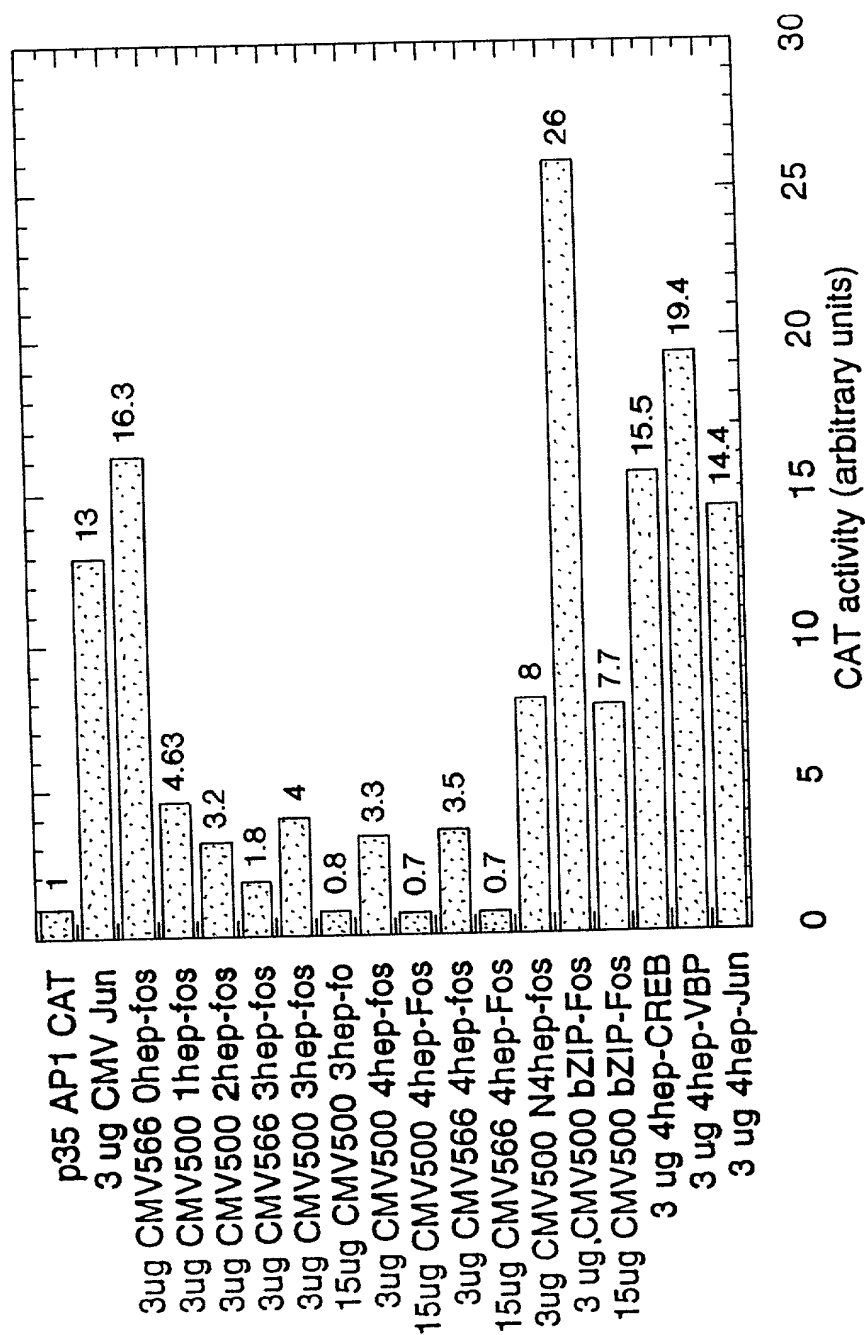
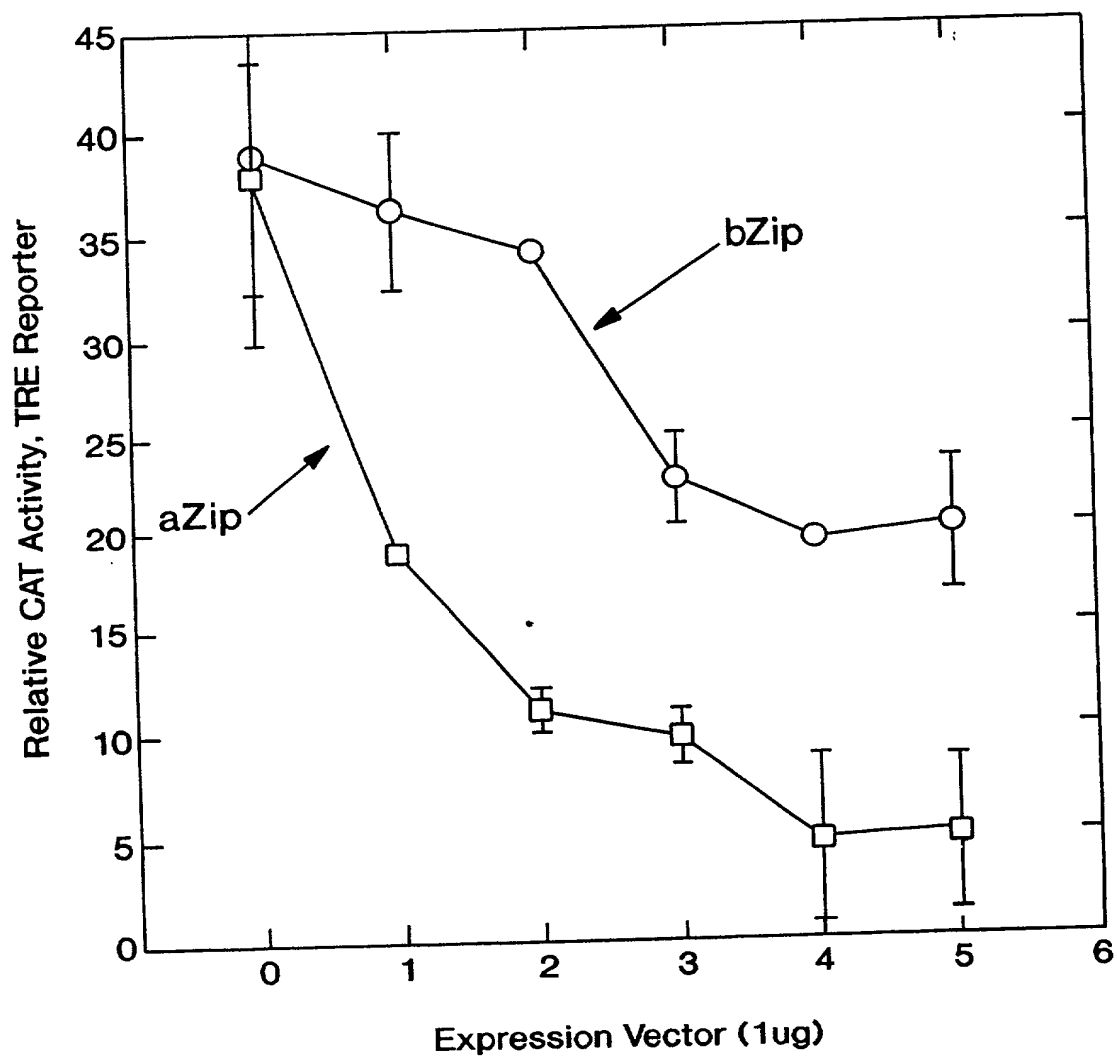


FIG. 7



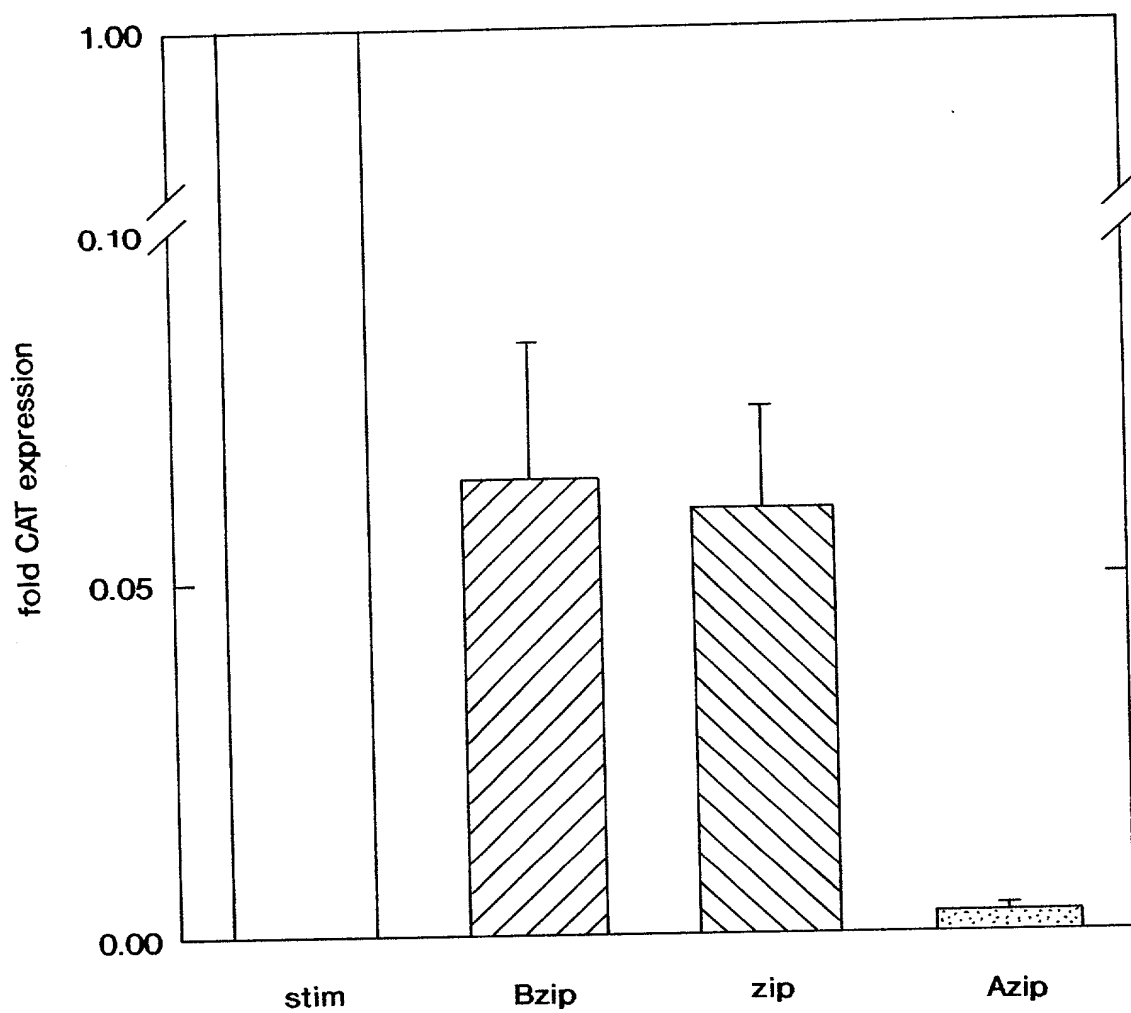


FIG. 8

FIG. 9

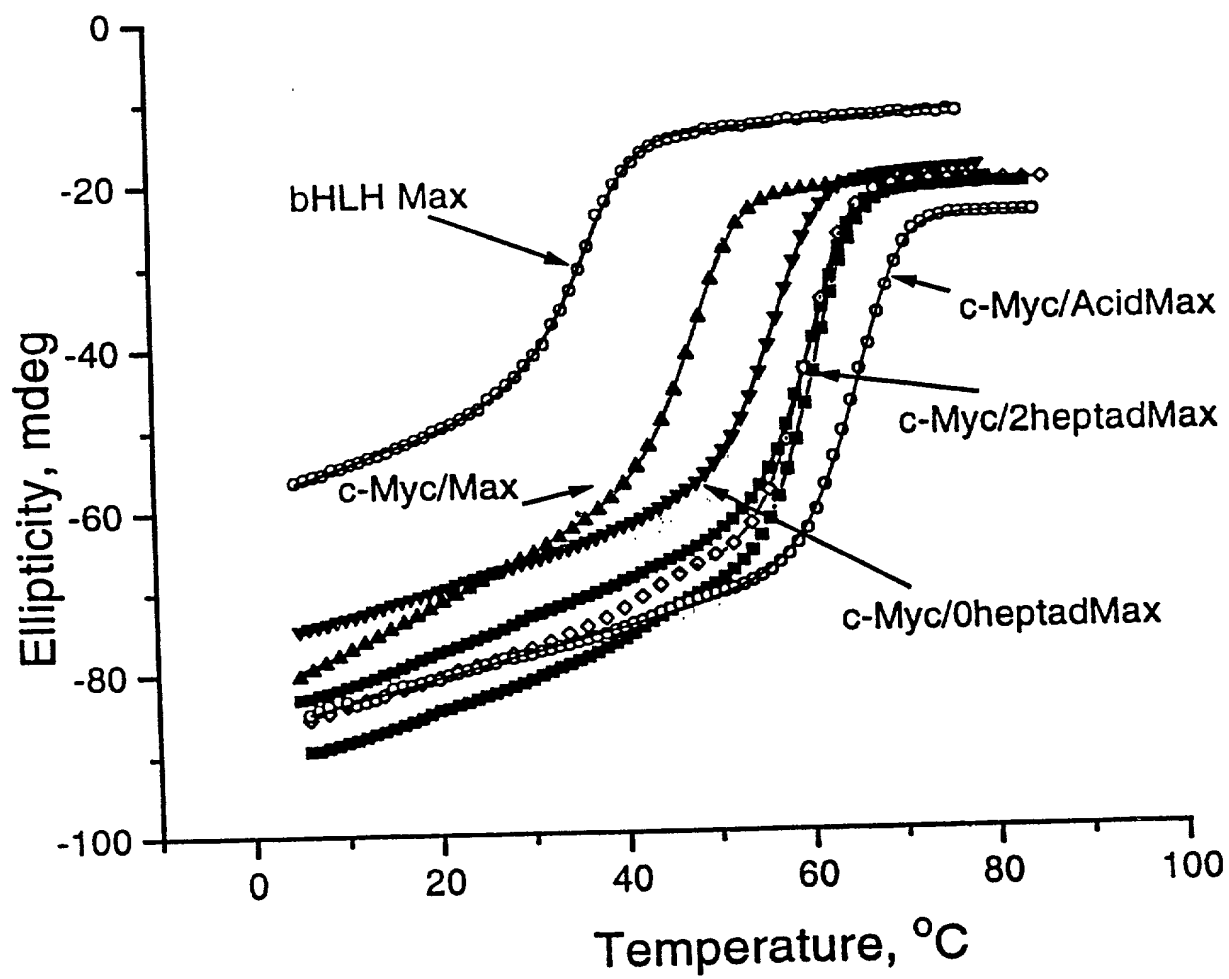


FIG. 10A

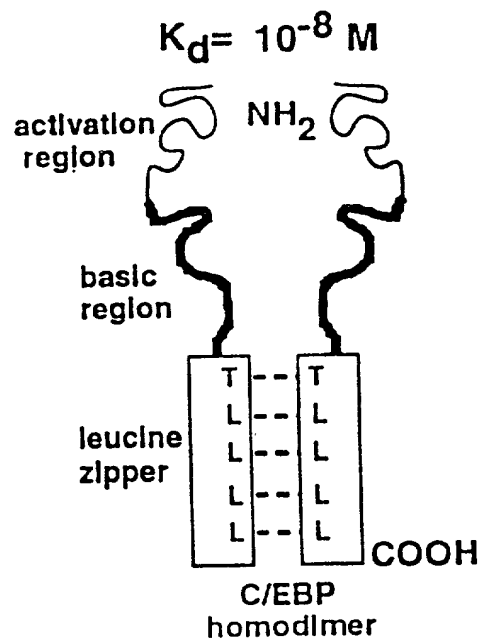


FIG. 10B

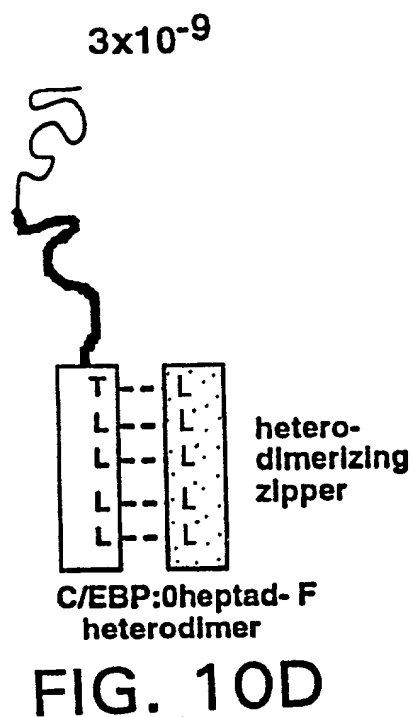
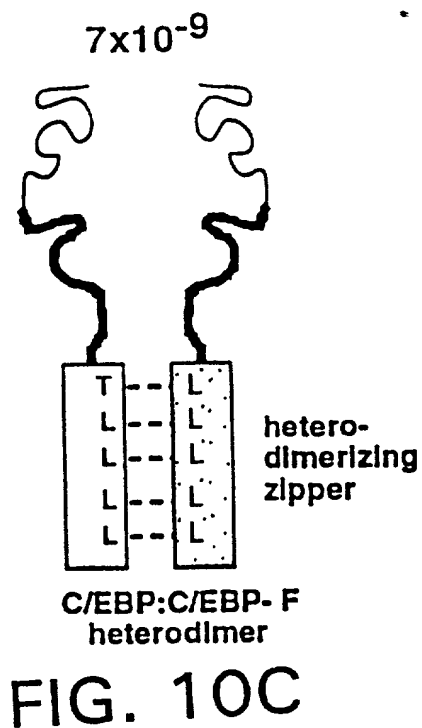
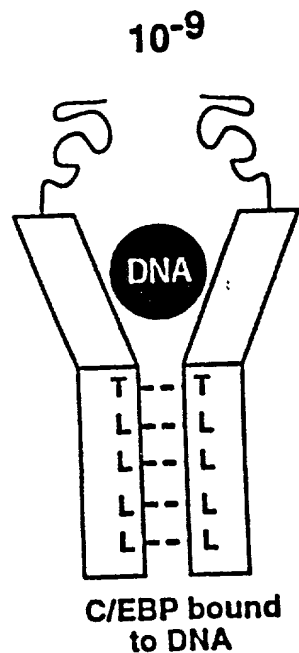


FIG. 11A

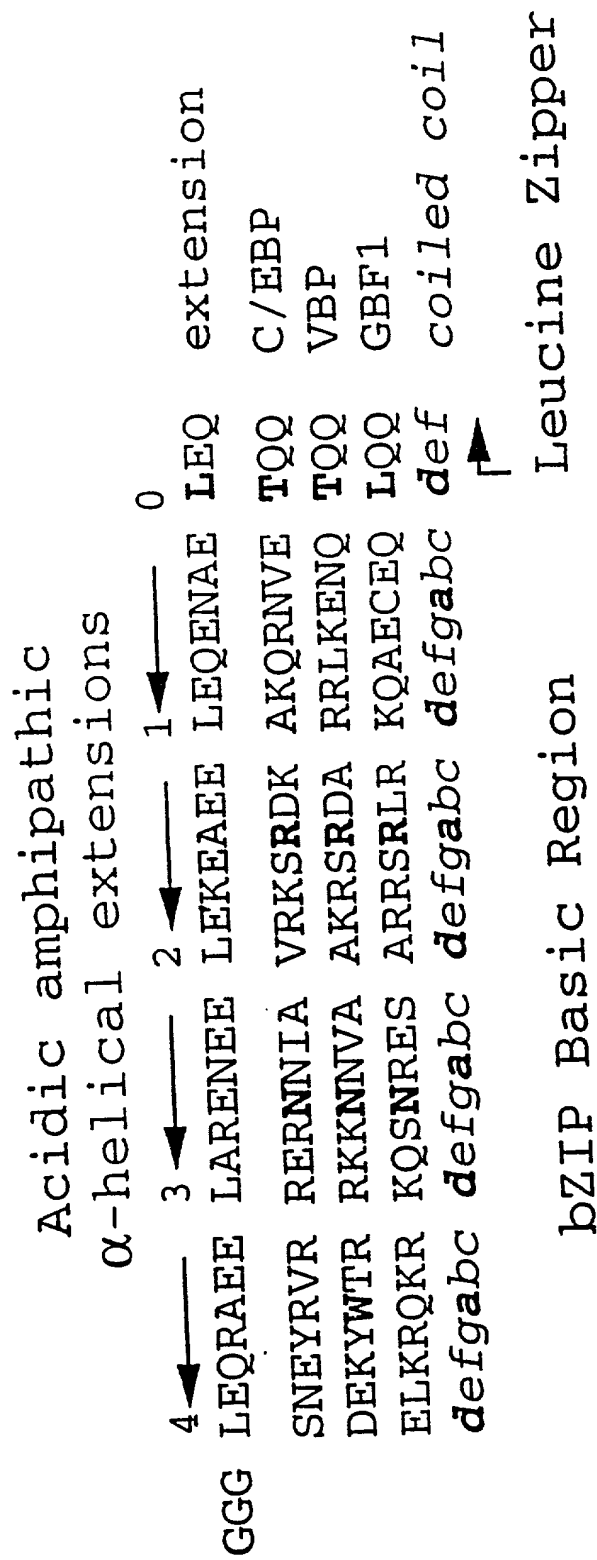


FIG. 11B

bZIP Basic Region

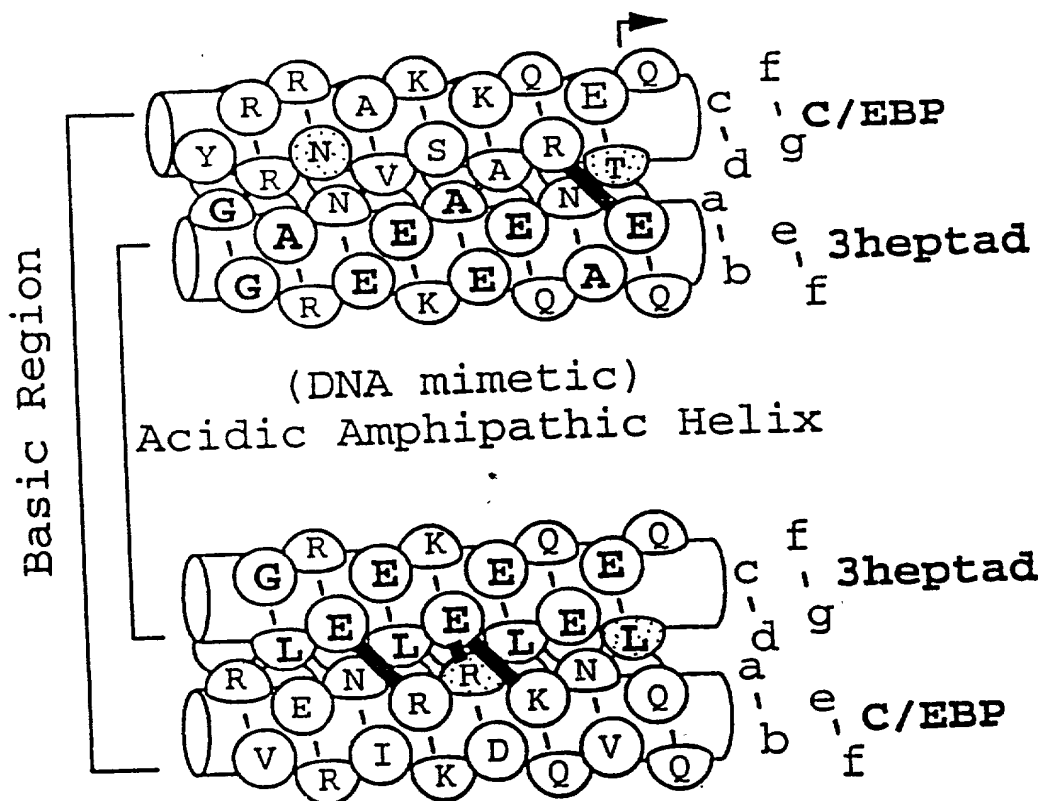


FIG. 11C

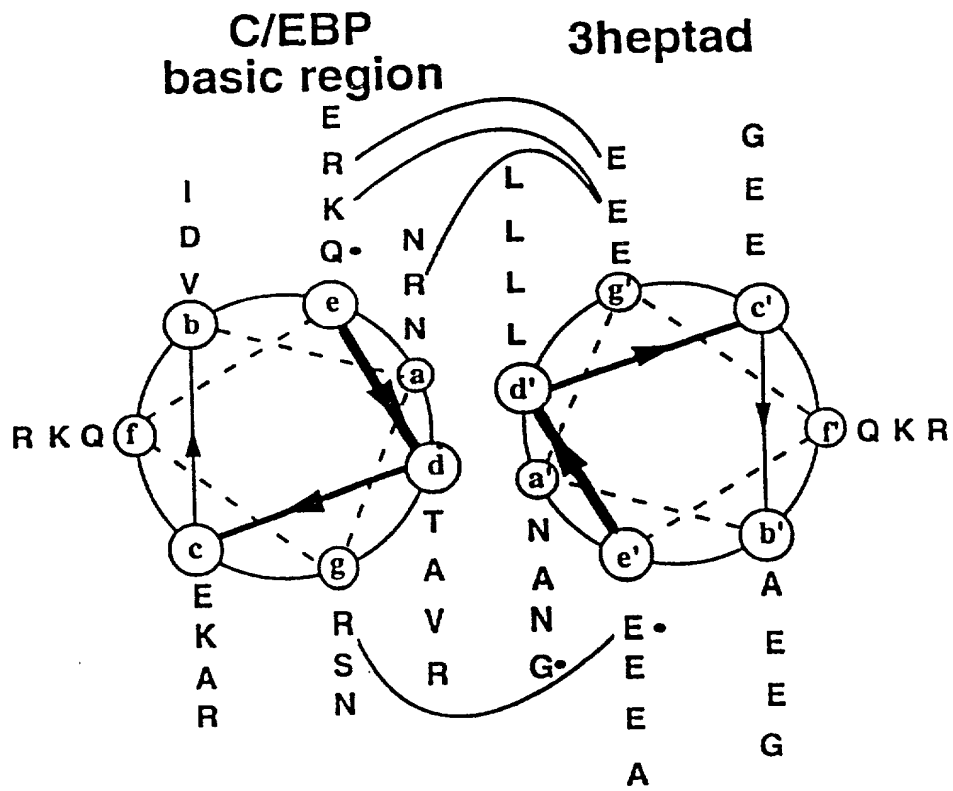


FIG. 12

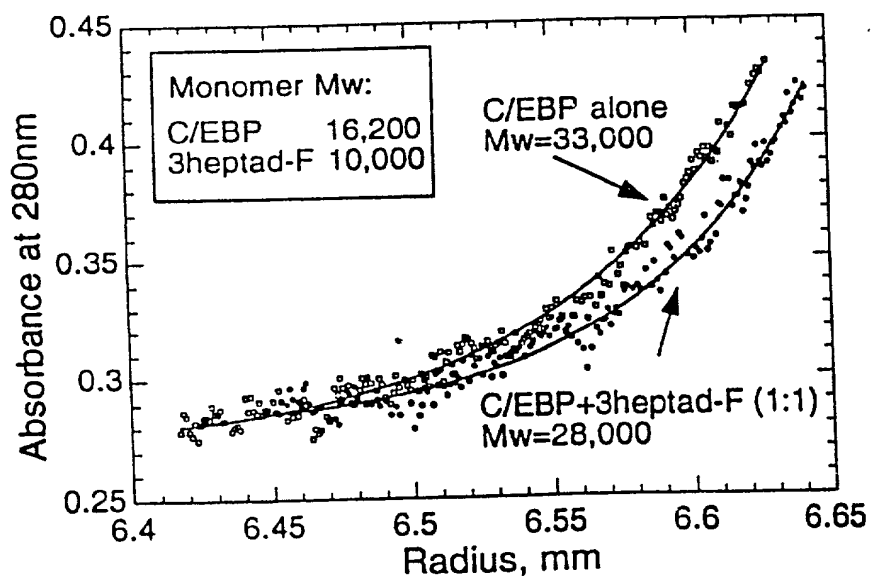


FIG. 13A

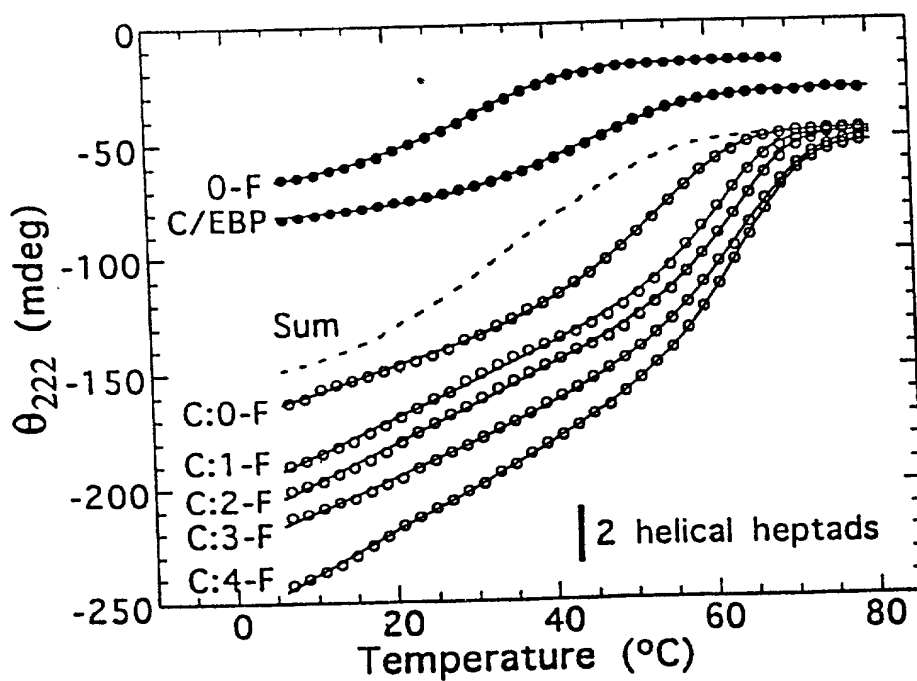
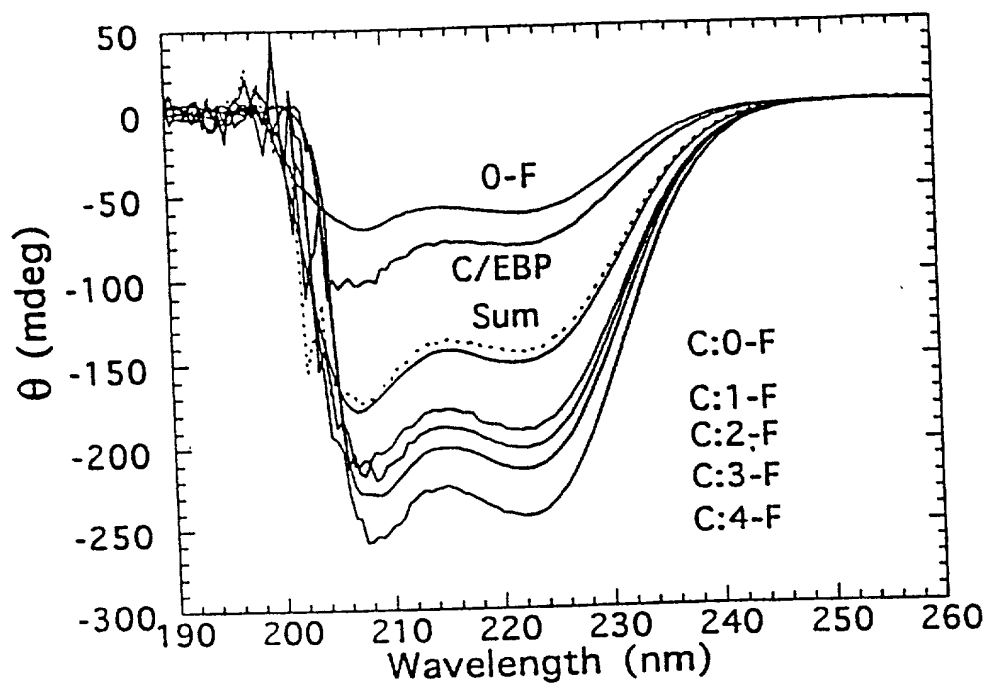


FIG. 13B

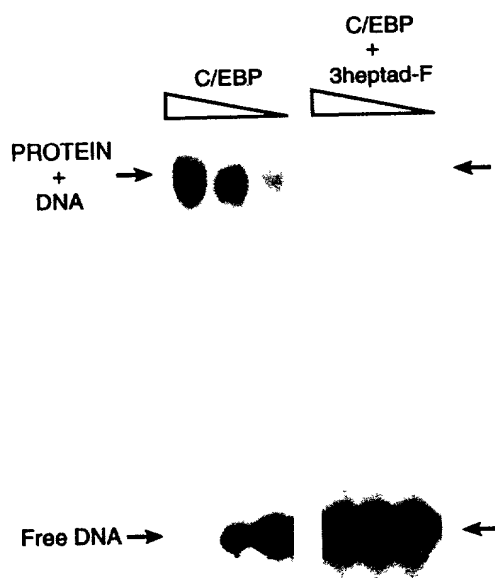


FIG. 14A

FIG. 14B

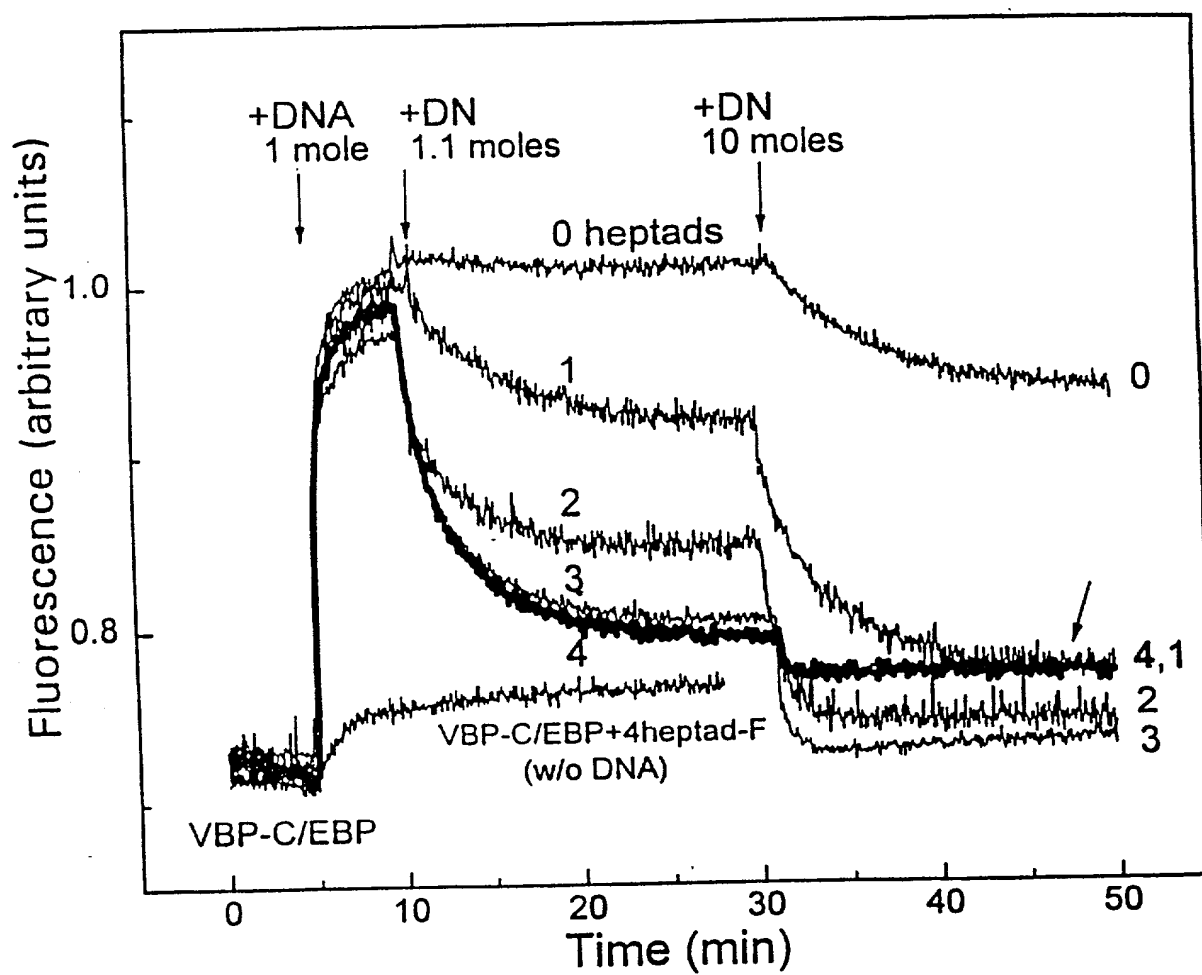


FIG. 15

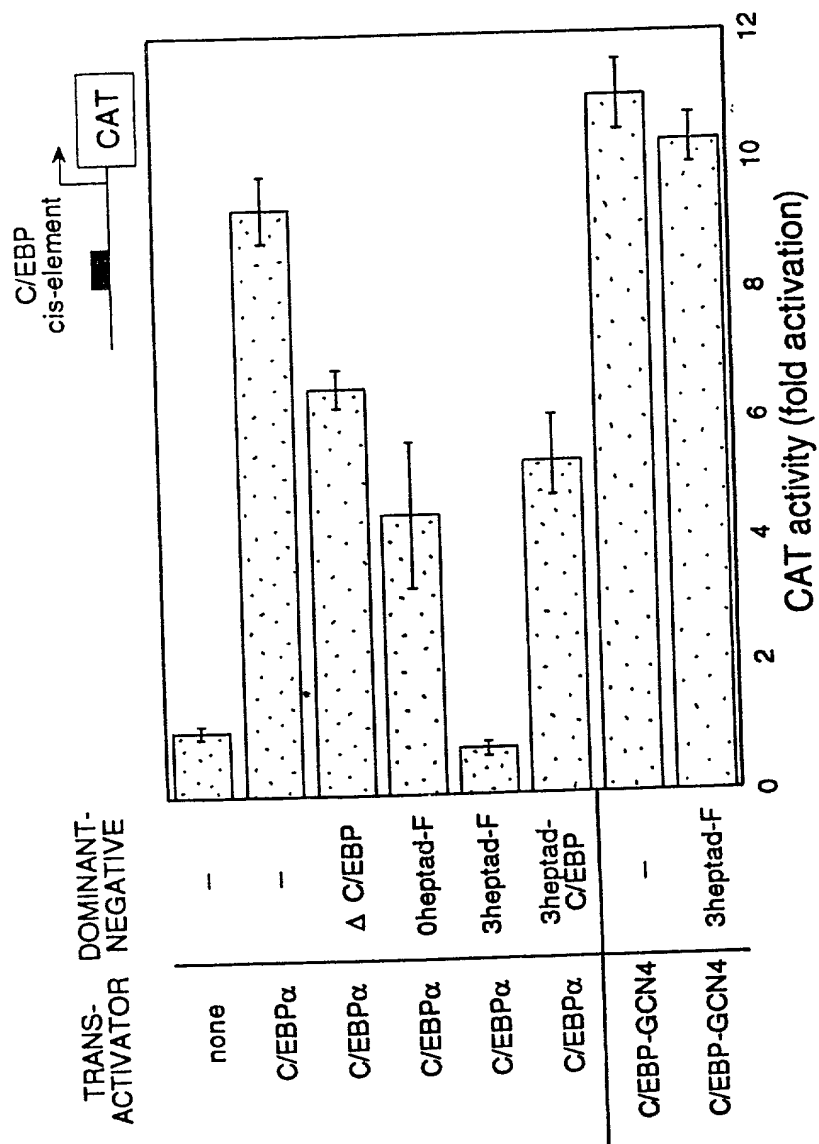
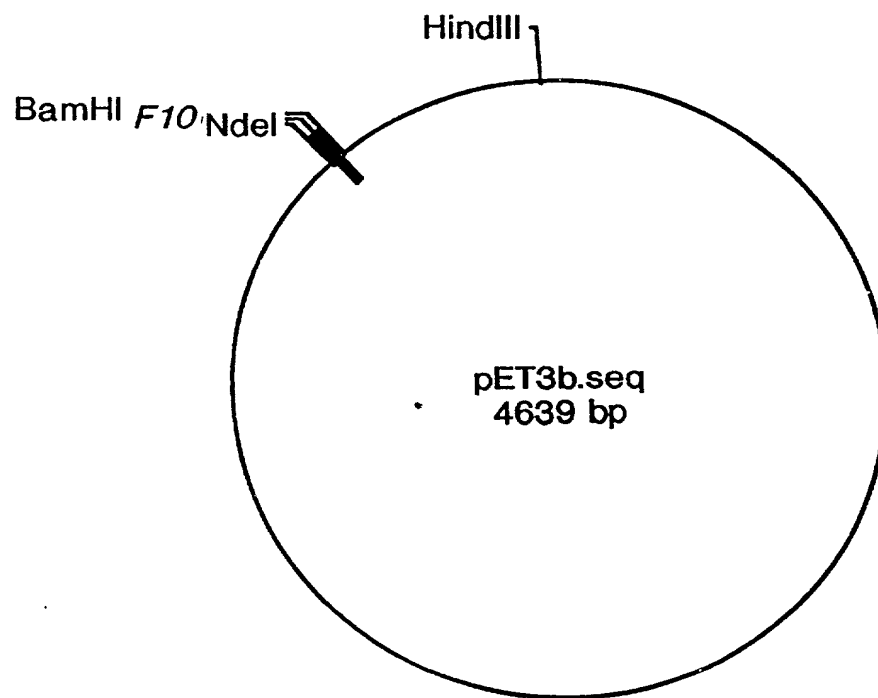


FIG. 16A



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FIG. 16B

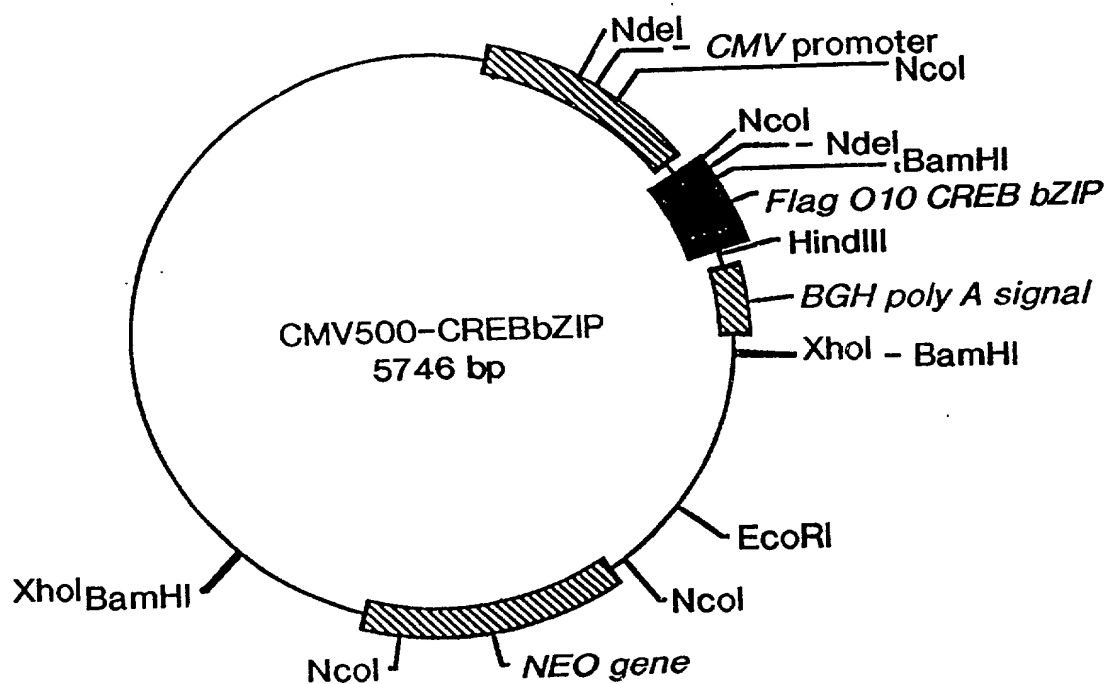
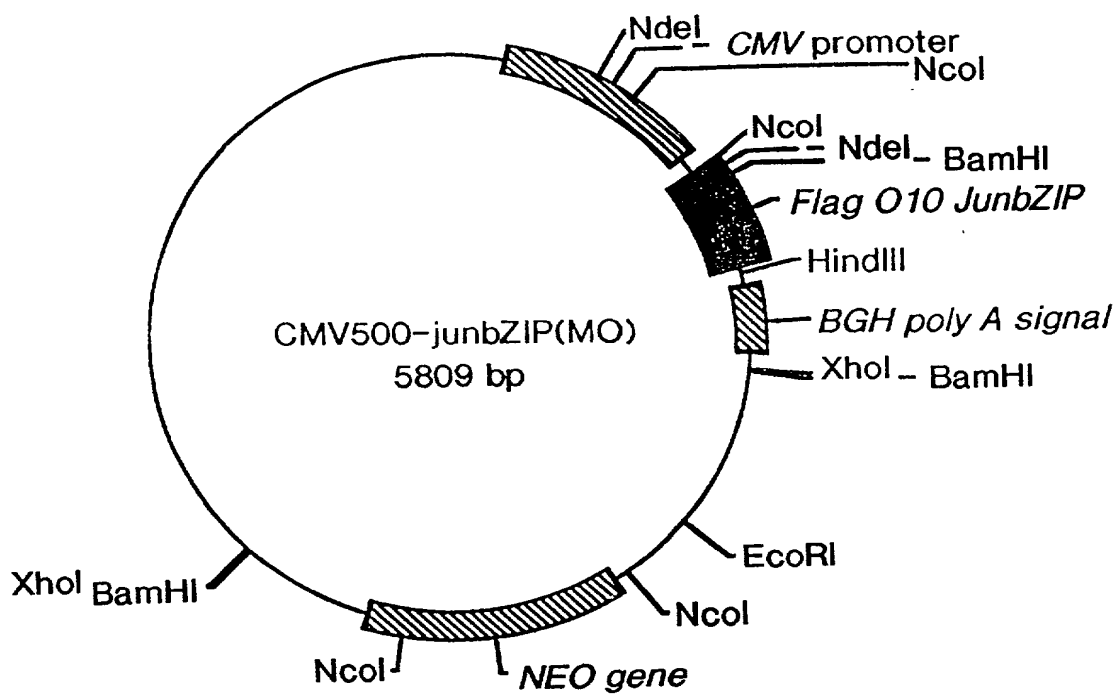


FIG. 16C

```

BamHI
GG ATCCC
10  *      *      *      *      *      *      *      *      *      *
   CCT ACA CAG CCT GCT GAA GAA GCA CGA AAG AGA GAG GTT CGT
   L P T Q P A E E A A R K R E V R>
   _a_CREB (AA 1-341); NCBI GI: 56005; CODON_START=1; _a_>

60  *      *      *      *      *      *      *      *      *      *
   CTA ATG AAG AAC AGG GAA GCA GCA AGA GAA TGT CGT AGA AAG AAG AAA
   L M K N R E A A R E C R R K K K>
   _a_CREB (AA 1-341); NCBI GI: 56005; CODON_START=1; _a_>

110 *      *      *      *      *      *      *      *      *      *
   GAA TAT GTG AAA TGT TTA GAG AAC AGA GTG GCA GTG CTT GAA AAC CAA
   E Y V K C L E N R V A V L E N Q>
   _a_CREB (AA 1-341); NCBI GI: 56005; CODON_START=1; _a_>

160 *      *      *      *      *      *      *      *      *      *
   AAC AAA ACA TTG ATT GAG GAG CTA AAA GCA CTT AAG GAC CTT TAC TGC
   N K T L I E E L K A L K D L Y C>
   _a_CREB (AA 1-341); NCBI GI: 56005; CODON_START=1; _a_>

200 *      *      *      *      *      *      *      *      *      *
   CAC AAG TCA GAT TAA TTC AAG CTT
   H K S D *>
   _CREB (AA 1-3_>

```

FIG. 17

900	910	920	930	940
* NcoI *	*	*	*	*
CC ATG GAC TAC AAG GAC GAC GAT GAC AAG CAT ATG GCT AGC ATG ACT GGT				
M D Y K D				
M D Y K D				
950	960	970	980	990
*	*	*	*	*
GGG CAG CAA ATG GGT CGG GAT CCC CTT CCT ACA CAG CCT GCT GAA GAA				
G Q Q M G R D D P L P T Q P A E E E>				
G Q Q M G R D D P L P T Q P A E E E>				
1000	1010	1020	1030	1040
*	*	*	*	*
GCA GCA CGA AAG AGA GAG GTT CGT CTA ATG AAG AAC AGG GAA GCA GCA				
A A R K R E V R L M K N R E A A>				
A A R K R E V R L M K N R E A A>				
1050	1060	1070	1080	1090
*	*	*	*	*
AGA GAA TGT CGT AGA AAG AAG AAA GAA TAT GTG AAA TGT TTA GAG AAC				
R E C R R K K K E Y V K C L E N>				
R E C R R K K K E Y V K C L E N>				
1100	1110	1120	1130	
*	*	*	*	*
AGA GTG GCA GTG CTT GAA AAC CAA AAC AAA ACA TTG ATT GAG GAG CTA				
R V A V L E N Q N K T L I E E L>				
R V A V L E N Q N K T L I E E L>				
1140	1150	1160	1170	1180
*	*	*	*	*
AAA GCA CTT AAG GAC CTT TAC TGC CAC AAG TCA GAT TAA TTC AAG CTT				
K A L K D L Y C H K S D *				
K A L K D L Y C H K S D *				

1170	*
1160	*
1150	*
1140	*
1180	*
* Hind III	

	910		920		930		940		D10
<u>NcoI</u> *	*	*	*	*	* <u>NdeI</u> *	*	*	*	*
CC ATG GAC	TAC AAG GAC GAC GAT GAC AAG CAT ATG	GCT AGC ATG ACT GGT							
M D Y K D D D D	K H M A S M T G>								
950	960	970	980	990					
*	*	* <u>BamHI</u> *	*	*	*	*	*	*	*
GGA CAG CAA ATG GGT CGG GAT CCT GAC CTG GAA CAA CGT GCT GAG GAA									
G Q Q M G R D D P D L E Q R A E E>									
1000	1010	1020	1030	1040					
*	*	*	*	*	*	*	*	*	*
CTG GCC CGT GAA AAC GAA GAG CTG GAA AAA GAG GCC GAA GAG CTG GAG									
L A R E N E E L E K E A E E L E>									
1050	1060	1070	1080	1090					
*	*	*	*	*	*	*	*	*	*
CAG GAA CTG GCA GAA CTC GAG AAC AGA GTG GCA GTG CTT GAA AAC CAA									
Q E L A E L E N R V A V L E N Q>									
1100	1110	1120	1130	1140					
*	*	*	*	*	*	*	*	*	*
AAC AAA ACA TTG ATT GAG GAG CTA AAA GCA CTT AAG GAC CTT TAC TGC									
N K T L I E E L K A L K D L Y C>									
1150	1160								
*	*	*	*	*	*	*	*	*	*
CAC AAG TCA GAT TAA TTC AAG CTT									
H K S D * F [K L>]									

Hind III

FIG. 19

2052720.012500

BamHI 10 20 30 40
* * * * *
GGATCCC AAG GTG GAA CAG TTA TCT CCA GAA GAA GAA GAG AAA AGG AGA
P D K V E Q>
L S P E E E E K R R>
____1783 TO ____>
____2470_2466 TO 2573 OF HUM FOS _0_b____>
50 60 70 80 90
* * * * *
ATC CGA AGG GAA AGG AAT AAG ATG GCT GCA GCC AAA TGC CGC AAC CGG
I R R E R N K M A A A K C R N R>
____2500_b____b____251_2466 TO 2573 OF HUM FOS _30_b____b____2540b____>
100 110 120 130 140
* * * * *
AGG AGG GAG CTG ACT GAT ACA CTC CAA GCG GAG ACA GAC CAA CTA GAA
R R E L T D T L Q A>
E T D Q L E>
____b_2_2466 TO 2573 OF HUM FOS _570b____>
26_2688 TO 3329 OF H____>
150 160 170 180 190
* * * * *
GAT GAG AAG TCT GCT TTG CAG ACC GAG ATT GCC AAC CTG CTG AAG GAG
D E K S A L Q T E I A N L L K E>
____2710_c____c____272_2688 TO 3329 OF HUM FOS _40_c____c____2750c____>
200 210 220 230 240
* * * * *
AAG GAA AAA CTA GAG TTC ATC CTG GCA GCT CAC CGA CCT GCC TGC AAG
K E K L E F I L A A H R P A C K>
____c_2760____c____c____2688 TO 3329 OF HUM FOS _2790____c____c____2800____>
250 260
* * * * *
ATC CCT GAT TAATTCAAGC TT
I P>
____c____>
Hind III

FIG. 20

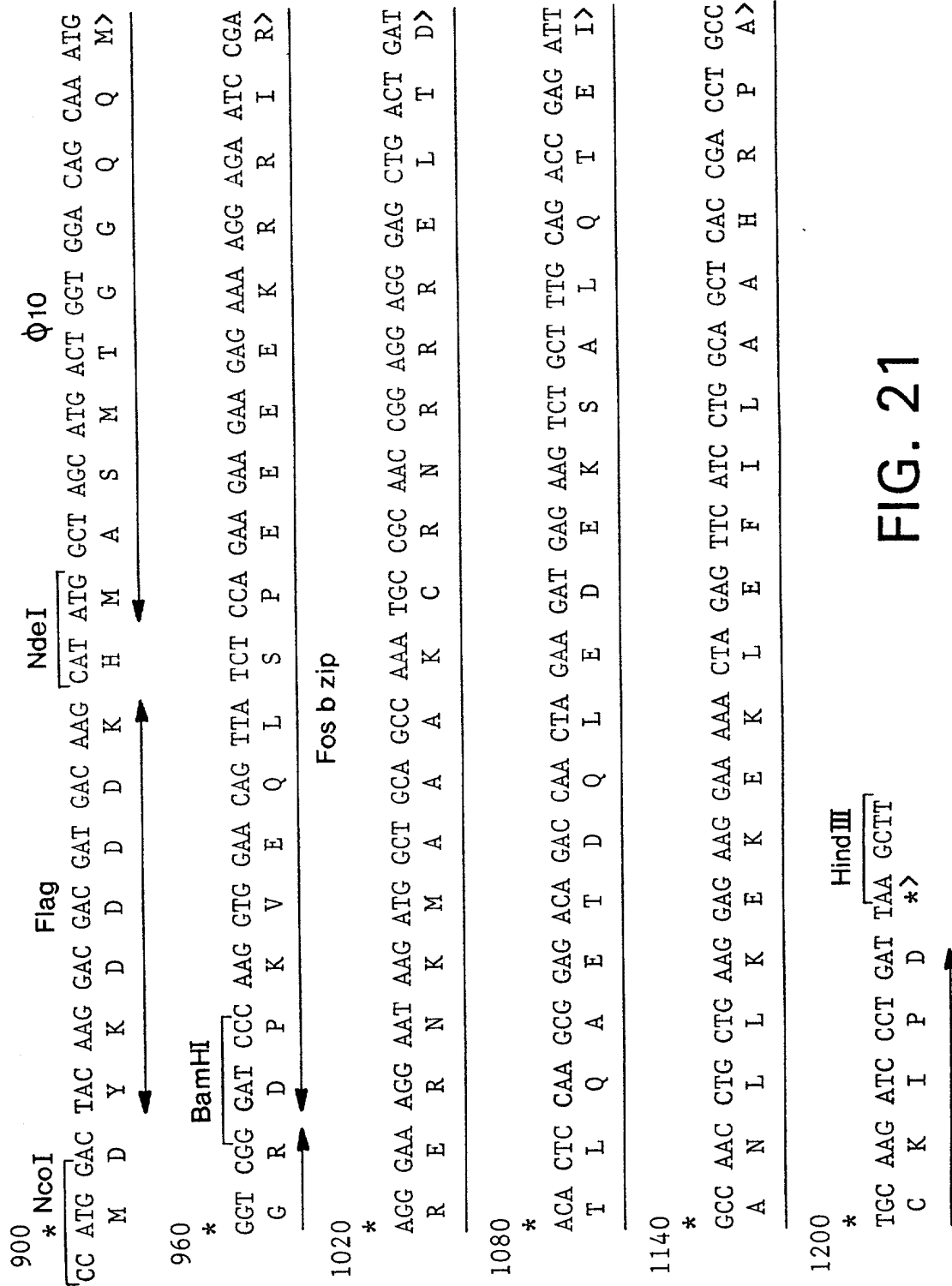


FIG. 21

FIG. 22

>NdeI

10 20 30 40 50

* * * * *

ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT

M A S M T G G Q Q M G R>

___a___a___a___a___a_F10___a___a___a___a___a___>

D P>

___b___>

60 70 80 90

* * * * *

GAC CTG GAA CAA CGT GCT GAG GAA CTG GCC CGT GAA AAC GAA GAG CTG

D L E Q R A E E L A R E N E E L>

___b___b___b___b___4HEPTAD ACIDIC EXTENSION___b___b___b___b___>

>XhoI

100 110 120 130 140

* * * * *

GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC GAG GCG

E K E A E E L E Q E N A E L E>

___b___b___b___b___4HEPTAD ACIDIC EXTENSION___b___b___b___b___>

A>

___>

150 160 170 180 190

* * * * *

GAG ACA GAC CAA CTA GAA GAT GAG AAG TCT GCT TTG CAG ACC GAG ATT

E T D Q L E D E K S A L Q T E I>

___c___c___c___c___c___C-FOS PROTEIN___c___c___c___c___c___>

200 210 220 230 240

* * * * *

GCC AAC CTG CTG AAG GAG AAG GAA AAA CTA GAG TTC ATC CTG GCA GCT

A N L L K E K E K L E F I L A A>

___c___c___c___c___c___C-FOS PROTEIN___c___c___c___c___c___>

>HindIII

250 260 270 280

* * * * *

CAC CGA CCT GCC TGC AAG ATC CCT GATT AATTCAAGCT T

H R P A C K I P>

___c___C-FOS PROTEIN___c___c___>

10059720.012900

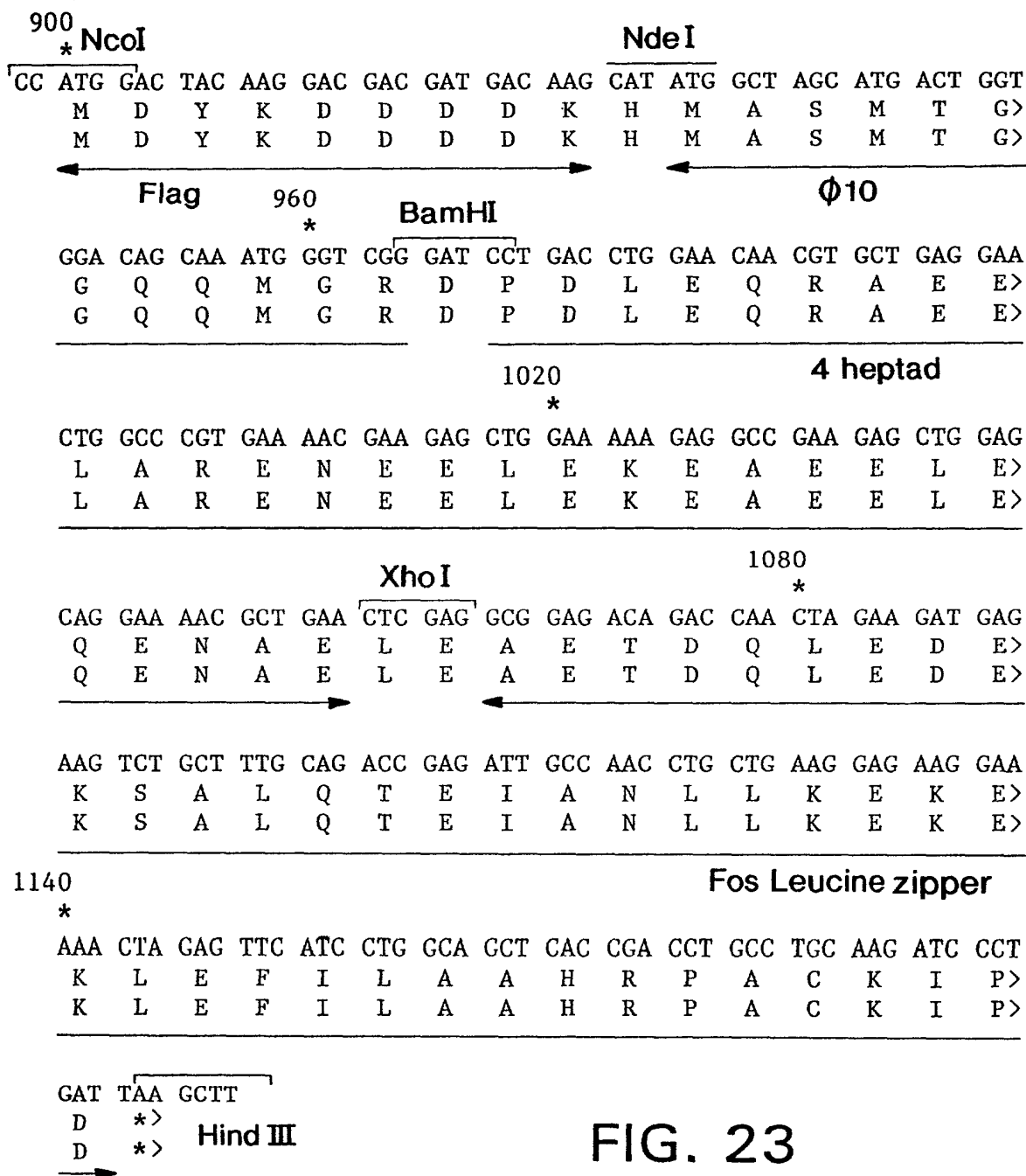


FIG. 23

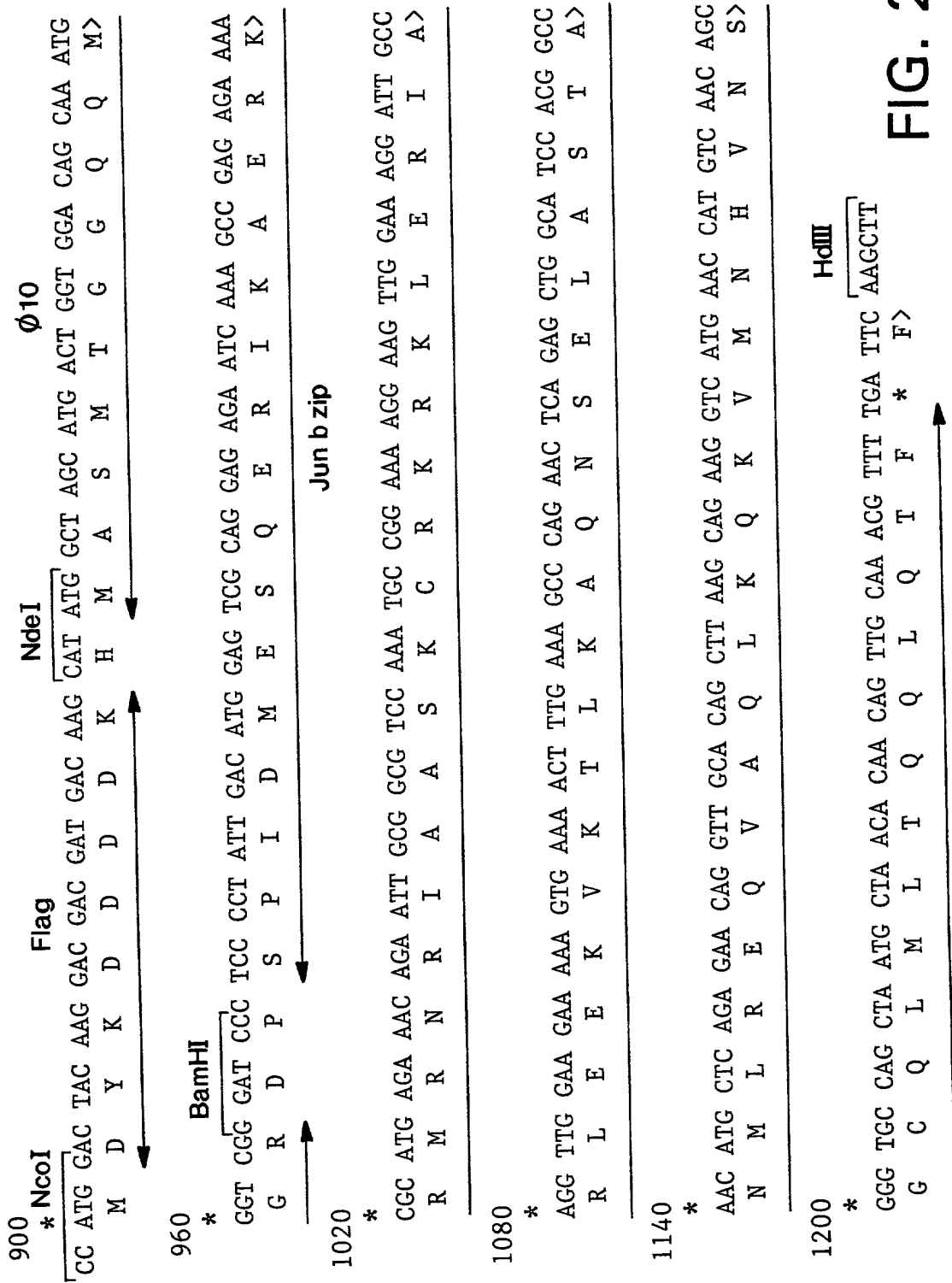


FIG. 24

FIG. 25

```

>NdeI
|
4090          4100          4110          4120          4130
* | * * * * *
ATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCC GAC
M A S M T G G Q Q M G R>
_a_a_a_a_a_F10_a_a_a_a_a>
D P D>
_b_b_b>

>XhoI
|
4140          4150          4160          4170          4180
* * * * *
GAA GAG GAA GAT GAC GAA GAA GAA CTC GAG GAA CTG GAA GAC AGC TTT
E E E D D E E E L E E L E>
_b_b_b_b_b_POLY-GLU_b_b_b_b_b>
D S F>
_c_c_c>

4190          4200          4210          4220          4230
* * * * *
CAC AGT TTG CGG GAC TCA GTC CCA TCA CTC CAA GGA GAG AAG GCA TCC
H S L R D S V P S L Q G E K A S>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c>

4240          4250          4260          4270
* * * * *
CGG GCC CAA ATC CTA GAC AAA GCA ACA GAG TAT ATC CAG TAT ATG CGA
R A Q I L D K A T E Y I Q Y M R>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c>

4280          4290          4300          4310          4320
* * * * *
AGG AAA AAC CAT ACG CAC CAG CAA GAC ATT GAT GAC CTC AAG CGG CAG
R K N H T H Q Q D I D D L K R Q>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c>

4330          4340          4350          4360          4370
* * * * *
AAT GCT CTT CTG GAG CAA CAA GTC CGT GCA CTG GAG AAG GCA AGA TCA
N A L L E Q Q V R A L E K A R S>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c>

>HindIII
|
4380          4390          4400
* * *
AGT GCC CAA CTG CAG ACC TGAGGCAA GCTTATC
S A Q L Q T>
_MAX BHLH DOMAIN_c>

```

10059720-012003

FIG. 26

```

>NdeI
|
4090      4100      4110      4120      4130
* | *      *      *      *      *
ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
      M  A  S  M  T  G  G  Q  Q  M  G  R>
      _a_a_a_a_a_F10_a_a_a_a_a_>
                                     D  P>
                                     _b_>

                                     >XhoI
                                     |
4140      4150      4160      4170
* | *      *      *      *      *
GAC CTG GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC
D  L  E  K  E  A  E  E  L  E  Q  E  N  A  E  L>
_b_b_TWO AMPHIPATHIC HEPTAD S (1st PHASE- 783) _b_b_>

4180      4190      4200      4210      4220
* | *      *      *      *      *
GAG CTG GAA GAC AGC TTT CAC AGT TTG CGG GAC TCA GTC CCA TCA CTC
E  L  E>
_b_b_>
      D  S  F  H  S  L  R  D  S  V  P  S  L>
      _c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_>

4230      4240      4250      4260      4270
* | *      *      *      *      *
CAA GGA GAG AAG GCA TCC CGG GCC CAA ATC CTA GAC AAA GCA ACA GAG
Q  G  E  K  A  S  R  A  Q  I  L  D  K  A  T  E>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4280      4290      4300      4310      4320
* | *      *      *      *      *
TAT ATC CAG TAT ATG CGA AGG AAA AAC CAT ACG CAC CAG CAA GAC ATT
Y  I  Q  Y  M  R  R  K  N  H  T  H  Q  Q  D  I>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4330      4340      4350      4360      4370
* | *      *      *      *      *
GAT GAC CTC AAG CGG CAG AAT GCT CTT CTG GAG CAA CAA GTC CGT GCA
D  D  L  K  R  Q  N  A  L  L  E  Q  Q  V  R  A>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

                                     >HindIII
                                     |
4380      4390      4400      4410      4420
* | *      *      *      *      *
CTG GAG AAG GCA AGA TCA AGT GCC CAA CTG CAG ACC TGA GGCAAGCTTA
L  E  K  A  R  S  S  A  Q  L  Q  T>
_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_>

```

FIG. 27

>NdeI
 4090 4100 4110 4120 4130
 * * * * *
 ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
 M A S M T G G Q Q M G R>
 _a_a_a_a_a_F10_a_a_a_a_a_>
 D P>
 b>

>BamHI
 4140 4150 4160 4170
 * * * * *
 GAC CTG GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC
 D L E K E A E E L E Q E N A E L>
 _b_b_TWO AMPHIPATHIC HEPTAD S (2ND PHASE- 784)_b_b_>

4180 4190 4200 4210 4220
 * * * * *
 GAG GAA CTG GAA GAC AGC TTT CAC AGT TTG CGG GAC TCA GTC CCA TCA
 E E L E>
 TWO AMPH>
 D S F H S L R D S V P S>
 _c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_>

4230 4240 4250 4260 4270
 * * * * *
 CTC CAA GGA GAG AAG GCA TCC CGG GCC CAA ATC CTA GAC AAA GCA ACA
 L Q G E K A S R A Q I L D K A T>
 _c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4280 4290 4300 4310 4320
 * * * * *
 GAG TAT ATC CAG TAT ATG CGA AGG AAA AAC CAT ACG CAC CAG CAA GAC
 E Y I Q Y M R R K N H T H Q Q D>
 _c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4330 4340 4350 4360 4370
 * * * * *
 ATT GAT GAC CTC AAG CGG CAG AAT GCT CTT CTG GAG CAA CAA GTC CGT
 I D D L K R Q N A L L E Q Q V R>
 _c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

>HindIII
 4380 4390 4400 4410 4420
 * * * * *
 GCA CTG GAG AAG GCA AGA TCA AGT GCC CAA CTG CAG ACC TGAGGCAAGC
 A L E K A R S A Q L Q T>
 _c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_>

TTATC

206270.02465001

FIG. 28

```

>NdeI
|
4090          4100          4110          4120          4130
* | *      *      *      *      *      *      *      *
ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
M A S M T G G Q Q M G R>
_a_a_a_a_a_F10_a_a_a_a_a_>
D P>
_b_>

>XhoI
|
4140          4150          4160          4170
* | *      *      *      *      *      *      *
GAC CTG GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC
D L E K E A E E L E Q E N A E L>
_b_b_TWO AMPHIPATHIC HEPTAD S (3D PHASE- 785) _b_b_>

4180          4190          4200          4210          4220
* | *      *      *      *      *      *      *
GAG GAA GAG CTG GAA GAC AGC TTT CAC AGT TTG CGG GAC TCA GTC CCA
E E E L E>
_TWO AMPHIPAT_>
D S F H S L R D S V P>
_c_c_c_MAX BHLH DOMAIN_c_c_c_>

4230          4240          4250          4260          4270
* | *      *      *      *      *      *      *
TCA CTC CAA GGA GAG AAG GCA TCC CGG GCC CAA ATC CTA GAC AAA GCA
S L Q G E K A S R A Q I L D K A>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4280          4290          4300          4310          4320
* | *      *      *      *      *      *      *
ACA GAG TAT ATC CAG TAT ATG CGA AGG AAA AAC CAT ACG CAC CAG CAA
T E Y I Q Y M R R K N H T H Q Q>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4330          4340          4350          4360          4370
* | *      *      *      *      *      *      *
GAC ATT GAT GAC CTC AAG CGG CAG AAT GCT CTT CTG GAG CAA CAA GTC
D I D D L K R Q N A L L E Q Q V>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

>HindIII
|
4380          4390          4400          4410          4420
* | *      *      *      *      *      *      *
CGT GCA CTG GAG AAG GCA AGA TCA AGT GCC CAA CTG CAG ACC TGAGGCA
R A L E K A R S S A Q L Q T>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

*
AGCTTATC

```

206210-02/6500

BamHI 10 20 30 40
 * * * * * *
 GGATCCC AAC GAC AAG AGG CGG ACA CAC AAC GTC TTG GAA CGT CAG AGG
 N D K R R T H N V L E R Q R>
 ___PUTATIVE; NCBI GI: 50468; CODON_START=1; C-MYC ___>

50 60 70 80 90
 * * * * * *
 AGG AAC GAG CTG AAG CGC AGC TTT TTT GCC CTG CGT GAC CAG ATC CCT
 R N E L K R S F F A L R D Q I P>
 ___PUTATIVE; NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;___>

100 110 120 130 140
 * * * * * *
 GAA TTG GAA AAC AAC GAA AAG GCC CCC AAG GTA GTG ATC CTC AAA AAA
 E L E N N E K A P K V V I L K K>
 ___PUTATIVE; NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;___>

150 160 170 180 190
 * * * * * *
 GCC ACC GCC TAC ATC CTG TCC ATT CAA GCA GAC GAG CAC AAG CTC ACC
 A T A Y I L S I Q A D E H K L T>
 ___PUTATIVE; NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;___>

200 210 220 230 240
 * * * * * *
 TCT GAA AAG GAC TTA TTG AGG AAA CGA CGA GAA CAG TTG AAA CAC AAA
 S E K D L L R K R R E Q L K H K>
 ___PUTATIVE; NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;___>

250 260 270
 * * * * *
 CTC GAA CAG CTT CGA AAC TCT GGT GCA TAA AAGCTT
 L E Q L R N S G A *> Hind III
 ___PUTATIVE; NCBI GI: 50468; CODON___>

FIG. 29

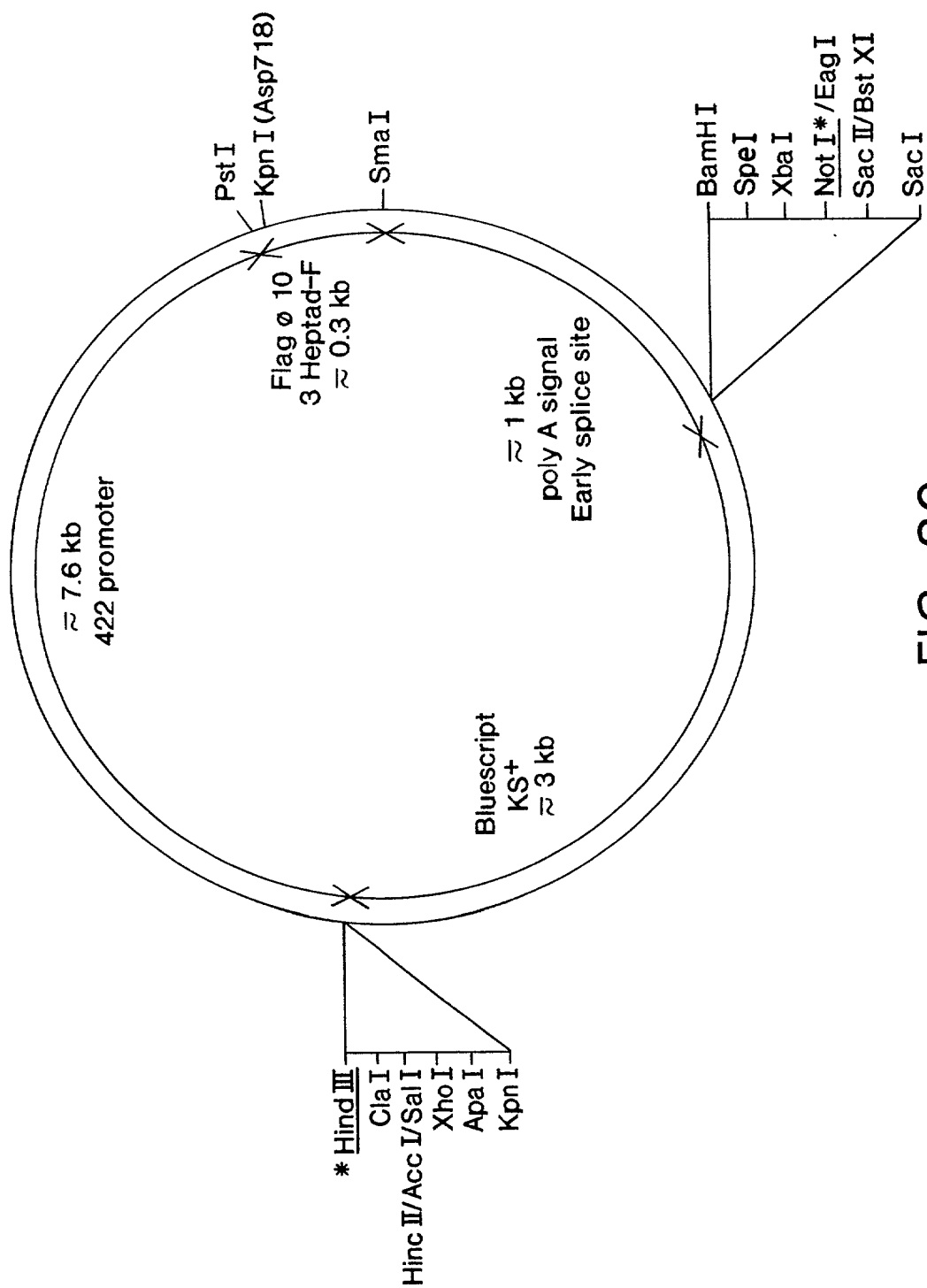


FIG. 30

A high-contrast, black and white photograph showing a small, light-colored object, possibly a mouse, on a dark, textured surface. The object is positioned in the lower-left quadrant of the frame. The background is dark and grainy, with a vertical line of light on the right side. The image is tilted slightly to the right.

FIG. 31